

SEQUENCE LISTING

<110> Rothschild, Max
Ciobanu, Dan
Malek, Massoud
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use of the Same as Genetic Markers for Reproductive and Meat Quality Traits

<130> P04668US3

<150> 60/231045
<151> 2000-09-08

<150> 60/260,239
<151> 2001-01-08

<150> 60/299,111
<151> 2001-06-18

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<170> PatentIn version 3.0

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344

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192

240

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130 135 140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	480
145 150 155 160	
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210 215 220	
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275 280 285	
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305 310 315 320	
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	1008
325 330 335	

DRAFT

gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340 345 350	1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355 360 365	1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370 375 380	1152
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gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu 420 425 430	1296
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Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
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Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
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Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
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Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
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Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
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His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
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Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
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225 230 235 240

D 6 6 2 2 2 2 2 2 2 2 2 2

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Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
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Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
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Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
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Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
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405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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 Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
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 Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
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 Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val
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 Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
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 Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
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 His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
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 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190

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 195 200 205

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Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc	768
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
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Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
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Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	
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gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc	1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly 35 40 45			
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln 50 55 60			
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu 65 70 75 80			
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp 85 90 95			
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110			

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Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
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Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
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Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
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Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
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Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
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Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
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Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
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Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
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Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
35 40 45

ccg agg gaa agt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag
Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
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gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
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gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624
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ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270	816
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gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300	912
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
35 40 45

Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

9950022000000000

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala

450

455

460

<210> 7
<211> 1873
<212> DNA
<213> Sus scrofa

<220>
<221> CDS
<222> (1)..(1392)

<400> 7
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Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

48

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

96

tct aga tgg aca agg gag gat gta gag gaa ggg ggg cct ccg ggc
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
35 40 45

144

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

192

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

240

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

288

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

336

ata gag ttc tca gcc tcg gcg tgg gat gag ctt ggg ctg gtg
Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

384

gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

432

ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

480

cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

528

aaa ctg gtc atc ttc gag acc atg ctg gag atc aag aag gcc ttc ttt
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe

576

0
0
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	180	185	190	
gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205				624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220				672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240				720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255				768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270				816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccc gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285				864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300				912
tcc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305 310 315 320				960
cgc acc atccaa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325 330 335				1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340 345 350				1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355 360 365				1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370 375 380				1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385 390 395 400				1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405 410 415				1248
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc				1296

DRAFT 22005990

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu		
420	425	430
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc		1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile		
435	440	445
ctt cag gct ctg gtg otc agc cct gct gga att gat gcc ctc ggg gcc		1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala		
450	455	460
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaaagcc agtgaaggga		1452
gccgtggact cagctctcac ttcccctcag ccccaacttgc tggctggct ctggcagg		1512
taggctccgc ccccccccccc tggcctcage atcagccccct cagttccctt gggcacccag		1572
atctcagact ggggcacccct gaagatggga gtggcccagc ttatagctga gcacccctgt		1632
gaaatctacc agcatcaaga ctcactgtgg gaccactgtt ttgtccatt ctcagctgaa		1692
atgatggagg gcctcataag aggggtggac agggccttgg atagaggcca gatcagtgc		1752
gtgccttcag gacccctccggg gagtttagagc tgccctctct cagttcagtt ccccccgt		1812
gagaatgtcc ctggaaaggaa gccagttaat aaaccttgg tggatggaat ttggagagtc		1872
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<211> 464
<212> PRT
<213> Sus scrofa

<400> 8

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala			
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala		
20	25	30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly		
35	40	45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln		
50	55	60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu			
65	70	75	80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp		
85	90	95

094002 000000

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val

325

330

335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
 420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
450 455 460

<210> 9
<211> 1873
<212> DNA
<213> Sus scrofa

<220>
<221> CDS
<222> (1) .. (1392)

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Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1           5                   10                  15

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gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
          20      25      30

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tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc
 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln

50

55

60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg
 Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

240

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac
 Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

288

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc
 Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

336

ata gag ttc tca gcc tcg gcg tcg ggg gat gag ctt ggg ctg gtg
 Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125

384

gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg
 Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140

432

ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg
 Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160

480

cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc
 His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175

528

aaa ctg gtc atc ttc gac acc atg ctg gag atc aag gcc ttc ttt
 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190

576

gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag
 Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys
 195 200 205

624

aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg
 Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
 210 215 220

672

ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa
 Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
 225 230 235 240

720

gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc
 Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
 245 250 255

768

aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc
 Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
 260 265 270

816

tac gcc ctc atc aag aac ccg atc cac cgc ctg ccg gtc ctg gac cct
 Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
 275 280 285

864

gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag ccg ctt ctc aag

912

0000000000000000

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys		
290	295	300
ttc ctg cac atc ttt ggc acc ctg ctg ccc cg ^g ccc tcc ttc ctc tac		960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr		
305	310	315
320		
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg		1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val		
325	330	335
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac		1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp		
340	345	350
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg		1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val		
355	360	365
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca		1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr		
370	375	380
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca		1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr		
385	390	395
400		
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg		1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly		
405	410	415
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc		1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu		
420	425	430
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc		1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile		
435	440	445
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc		1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala		
450	455	460
tgagaaccttgc ctctcaggcc acctggcaca cctggaaagcc agtgaaggaa		1452
gcggctggact cagctctcac ttccccctcag ccccaacttgc ttgtctggct ctgttcagg		1512
taggtcccgcc cggggggcccc tggcctcagc atcagccccct cagtctccct gggcaccccg		1572
atctcagact ggggcacccct gaagatggga gtggcccagc ttatactgaa gcagccttgt		1632
gaaaatctacc agcatcaaga ctcaactgtgg gaccactgtct ttgtcccttctt ctcagatgaa		1692
atgatggagg gcctcataag aggggtggac agggcctggaa gttagaggcca gatcgtgac		1752
gtgccttcag gacctccggg gagtttagac tgccctctct cagttcagtt ccccccgtct		1812
gagaatgtcc ctgaaaggaa gccagttaat aaaccttggt tggatggaaat ttggagagtc		1872

<210> 10
<211> 464
<212> PRT
<213> Sus scrofa

<400> 10

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
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Ser Arg TriP Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys

195

200

205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
 210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
 225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
 245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
 260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
 275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
 290 295 300

Phe Leu His Ile Phe GLY Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
 305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
 325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
 340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
 355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
 370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
 405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
 420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
450 455 460

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<211> 1095
<212> DNA
<213> Sus scrofa

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cttctttgtt ccgcctttgtt tcttcttctt ccctcttccct caccccttccctt ctctttcaaa 240
agagtagagg gggcatctat agagtctggta gattgggact ctcttgactt tctcgcttac 300
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ggggcaggca ccgaacctgc aacctcatgg ttccctagtg gatcgatccaa ccactgcgcc 720
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tgttactccc cattaaccaa acaggccccat ttctcccttg cagagatgag ttcccttagag 840
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ggggaccagg ggaccaaggc ctcttagatgg acaaggccagg agatgtttaga ggaagggggg 960
ctcccgcccgcc cgaggaaarg tgagttcaag ggcaggatctg gggagctggg actggggggca 1020
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taacatcatg cagcc 1095

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<211> 808
<212> DNA

1400-13

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cttctttgtt ccgtttgtt tttttttctt ccttcttcctt cacccttcctt cttttcaaa	240
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tagctgtgtg attttgtggca aattgtttca cctctctgag ctcaggcttc tcgttagtaa	360
aacagggtct atagccatgc ctttcggata agattgccgt gagggttcaa tgagaattt	420
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atgaaatttta ttgtgttact cccctttaac caaacagggtc ccattctccc ttgcagagat	540
gagtttcata gagcaaggag agagccgttc atggccatcc cgagctgtga ccaccagctc	600
agaaaagaagc catggggacc aggggacca ggcctctaga tggacaaggc aggaggat	660
agaggaaggg gggctccgg gcccggggaa argtgagttc aaggccagtt ctggggagct	720
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<210> 14	
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<212> DNA	
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